

## REPLACEMENT SHEET

### FIGURE 4

**A.**

**SEQ ID NO:63 - AME 5 light chain variable region amino acid sequence**

DIQMTQSPSSLSASVGDRVTITCRASSSVHYIHWYQQKPGKVPKLLIYATSGLAS  
GVPSRFSGSGSGTDFTLTISLQPEDVATYYCQTWTFNPPTFGGGTKVEIK

**B.**

**SEQ ID NO:64 - AME 5 light chain variable region nucleic acid sequence**

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGA  
GACAGAGTCACCATCACTTGCAGGGCCAGCTCAAGTGTACATTACATC  
CACTGGTACCAGCAGAAACCAGGGAAAGTTCCTAAGCTCTTGATCTAT  
GCCACATCCGGCCTGGCTTCTGGGGTCCCATCTCGGTTCAGTGGCAGT  
GGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAA  
GATGTTGCCACTTATTACTGCCAGACTTGGACTTTTAACCCTCCCACG  
TTCGGCGGAGGGACCAAGGTGGAGATCAAA

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### FIGURE 5

**A.**

**SEQ ID NO:65 - AME 5 heavy chain variable region amino acid sequence**

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYNMHWVRQAPGQGLEWMGAIY  
PGNGDTSYNQKFKWRVTMTRDTSTSTVYMELSSLRSEDVAVYYCARSTYYGGD  
WQFDEWGKGTTVTVSS

**B.**

**SEQ ID NO:66 - AME 5 heavy chain variable region nucleic acid sequence**

CAGGTGCAGCTGGTGCAGTCTGGTGCTGAAGTGAAGAAGCCTGGGGCC  
TCAGTGAAGGTGTCCTGCAAGGCATCTGGATACACCTTCACCAGCTAC  
AATATGCACTGGGTGCGACAGGCCCTGGACAAGGGCTTGAGTGGATG  
GGAGCCATCTATCCTGGAAATGGTGATACAAGCTACAATCAGAAGTTT  
AAATGGAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTAC  
ATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGT  
GCGAGATCGACTTATTACGGCGGTGACTGGCAGTTCGACGAGTGGGGC  
AAAGGGACCACGGTCACCGTCTCCTCA

ANNOTATED SHEET- Deleted Figure 8

**FIGURE 8**

**A. Amino acid sequence of a human light chain framework region Vkl (DPK4)  
(A20) with interspersed CDR sequences labeled**

—————(FRL1-SEQ ID NO:87)—————(CDRL1)—————(FRL2-SEQ ID NO:88)—————(CDRL2)  
DIQMTQSPSSLSASVGDRVTITCXXXXXXXXXXXXWYQQKPGKVPKLLIYXXXXXXXX  
  
—————(FRL3-SEQ ID NO:89)—————(CDRL3)—————(FRL4-SEQ ID NO:90)—————  
GVPSRFGSGSGTDFLTITSSLPEDVATYYCXXXXXXXXXXFGGGTKVEIK

**B. Nucleic acid sequence of a human light chain framework region Vkl (DPK4)  
(A20) with interspersed CDR sequences labeled**

—————(FRL1-SEQ ID NO:91)—————  
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAG  
  
—————(CDRL1)—————  
TCACCATCACTTGCXXXXXXXXXXXXXXXXXXXXXXXXXXXXTGGTACCAG  
  
—————(FRL2-SEQ ID NO:92)—————(CDRL2)—————  
CAGAAACCAGGGAAAGTTCCTAAGCTCTTGATCTATXXXXXXXXXXXXXXXXXXXX  
  
(CDRL2 cont.)—————(FRL3-SEQ ID NO:93)—————  
XXXXGGGGTCCCATCTCGGTTCACTGGCAGTGGATCTGGGACAGATTTCACTCT  
  
CACCATCAGCAGCCTGCAGCCTGAAGATGTTGCCACTTATTACTGCXXXXXXXXXX  
  
—————(CDRL3)—————(FRL4-SEQ ID NO:94)—————  
XXXXXXXXXXXXXXXXXXXXTTCCGGCGGAGGGACCAAGGTGGAGA

TCAAA

ANNOTATED SHEET- Deleted Figure 9

**FIGURE 9**

**A. ~~Amino acid sequence of a human heavy chain framework region VHI DP7/21-2~~**  
**~~with interspersed CDR sequences labeled~~**

—————(FRH1—SEQ ID NO:95)—————(CDRH1)—————(FRH2—SEQ ID NO:96)  
QVQLVQSGAEVKKPGASVKVSCKASXXXXXXXXXXWVRQAPGQGLEWMG

—————(CDRH2)—————(FRH3—SEQ ID NO:97)—————  
XXXXXXXXXXXXXXXXXXRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR

—————(CDRH3)—————(FRH4—SEQ ID NO:98)  
XXXXXXXXXXXXXWGKGTTTVSS

**B. ~~Nucleic acid sequence of a human heavy chain framework region VHI DP7/21-2~~**  
**~~with interspersed CDR sequences labeled~~**

—————(FRH1—SEQ ID NO:99)  
CAGGTGCAGCTGGTGCAGTCTGGTGCTGAAGTGAAGAAGCCTGGGGCCTCAGTG

—————(CDRH1)—————  
AAGGTGTCCTGCAAGGCATCTXXXXXXXXXXXXXXXXXXXXXXXXXXXXTG

—————(FRH2—SEQ ID NO:100)—————(CDRH2)  
GGTGCGACAGGCCCTGGACAAGGGCTTGAGTGGATGGGAXXXXXXXXXXXX

—————(CDRH2 cont.)—————  
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXAGAGTCACCATGAC

—————(FRH3—SEQ ID NO:101)  
CAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGCCTGAGATCTGA

—————(CDRH3)—————  
GGACACGGCCGTGTATTACTGTGCGAGAXXXXXXXXXXXXXXXXXXXXXXXXXXXX

—————(CDRH3)—————(FRH4—SEQ ID NO:102)  
XXXXXXXXXXTGGGGCAAAGGGACCACGGTCACCGTCTCCTCA

## REPLACEMENT SHEET

### FIGURE 6

**A.**

**SEQ ID NO:67 - AME 33 complete light chain amino acid sequence**

EIVLTQSPGTLSPGERATLSCRASSVPYIHWYQQKPGQAPRLLIYATSALASGIPDR  
FSGSGSGTDFTLTISRLEPEDFAVYYCQQWLSNPPTFGQGTKLEIKRTVAAPSVFIFPPS  
DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS  
TYLSSTLTLSKADYEEKHKVYACEVTHQGLSSPVTKSFNRGEC

- Constant Region is underlined

**B.**

**SEQ ID NO:68 - AME 33 complete light chain nucleic acid sequence**

GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAG  
CCACCCTCTCCTGCAGGGCCAGCTCAAGTGTACCGTACATCCACTGGTACCAGCA  
GAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGCCACATCCGCTCTGGCTTCTG  
GCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCAT  
CAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTGGCTGAGT  
AACCACCCACTTTTGGCCAGGGGACCAAGCTGGAGATCAAACGAACTGTGGCTG  
CACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTCC  
TCTGTTGTGTGCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGA  
AGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA  
CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAGCAGA  
CTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCG  
CCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG

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### FIGURE 7

#### A. SEQ ID NO:69 - AME 33 complete heavy chain amino acid sequence

EVQLVQSGAEVKKPGESLKISCKGSGRTFTSYNMHWVRQMPGKGLEWMGAIYPLTG  
DTSYNQKSKLQVTISADKSISTAYLQWSSLKASDTAMYCARSTYVGGDWQFDVWG  
KGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS  
GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH  
TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV**D**GV  
EVHNAKT**K**PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA  
KGQPREPQVYTLPSRDELTKNQVSLTCLVKGFYPSDIAVESNGOPENNYKTTPPV  
LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

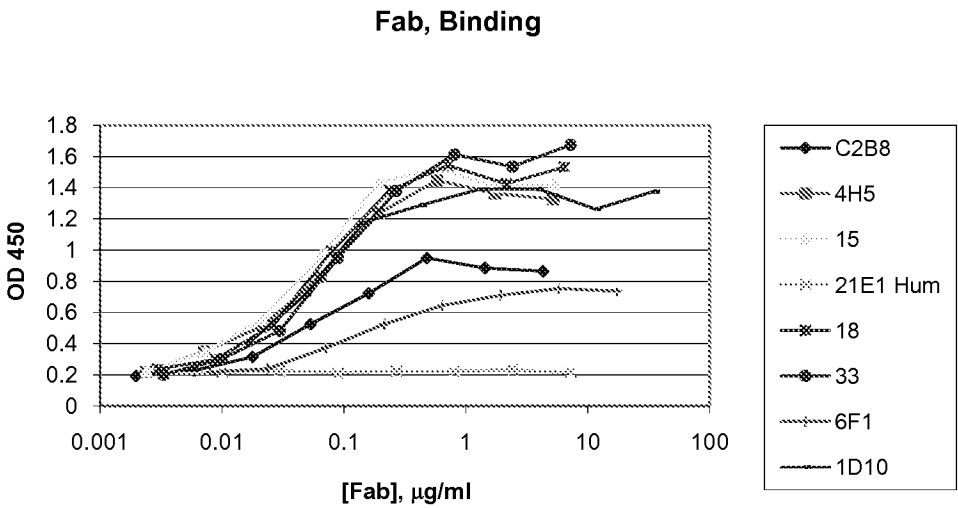
- Constant Region is underlined; the "D" at position 280 and "K" at position 290 are in bold

#### B. SEQ ID NO:70 - AME 33 complete heavy chain nucleic acid sequence

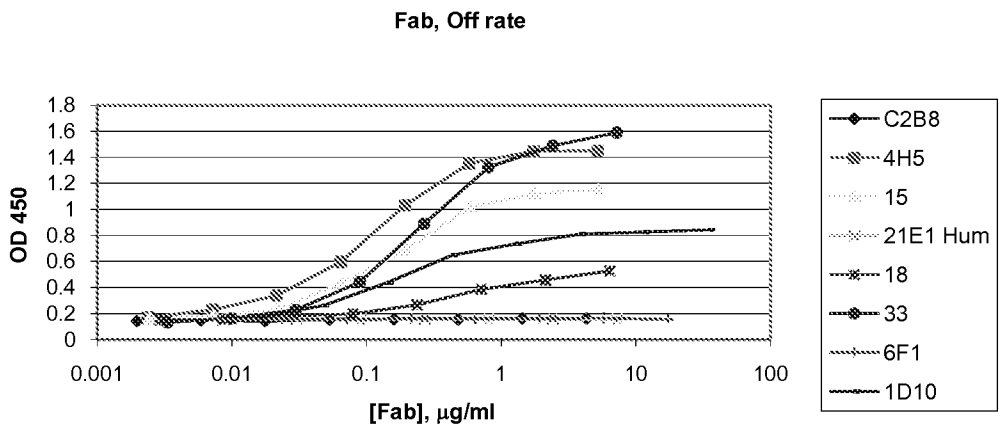
GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCCGGGGAGTCTCTG  
AAGATCTCCTGTAAGGGTCTGGCCGTACATTTACCAGTTACAATATGCACTGGGT  
GCGCCAGATGCCCGGAAAGGCCTGGAGTGGATGGGGGCTATTTATCCCTTGACG  
GGTGATACTTCCTACAATCAGAAGTCGAAACTCCAGGTCACCATCTCAGCCGACA  
AGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAAGGCCTCGGACACCGC  
CATGTATTACTGTGCGAGATCGACTTACGTGGGCGGTGACTGGCAGTTCGATGTCT  
GGGGCAAGGGGACCACGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGT  
CTTCCCCCTGGCACCCTCCTCCAAGAGCACCCTCTGGGGGCACAGCGGCCCTGGGT  
GCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAAGTCAAGGCGC  
CCTGACCAGCGGCGTGACACCTTCCCGGCTGTCTACAGTCCTCAGGACTCTACT  
CCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACAT  
CTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAGGTTGAGCC  
CAAATCTTGACAAAACCTCACACATGCCACCGTGCCAGCACCTGAATCCTG  
GGGGGACCGTCAGTCTTCTTCCCCCAAAACCCAAGGACACCTCATGATCTC  
CCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAG  
GTCAAGTTCAACTGGTACGTG**GAC**GGCGTGGAGGTGCATAATGCCAAGACAAAG  
CCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAAGGTCTCCAACAAAG  
TGCAACGAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAG  
CCCTCCCAGCCCCATCGAGAAAACCATCTCCAAGGCCAAAGGGCAGCCCCGAGA  
ACCACAGGTGTACACCCTGCCCCATCCCGGGACGAGCTGACCAAGAACCAGGTC  
AGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGG  
AGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTGCTGGACTC  
CGACGGCTCCTTCTTCTCTATAGCAAGCTACCGTGGACAAGAGCAGGTGGCAG  
CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACA  
CGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA

FIGURE 8

A.



B.



C.

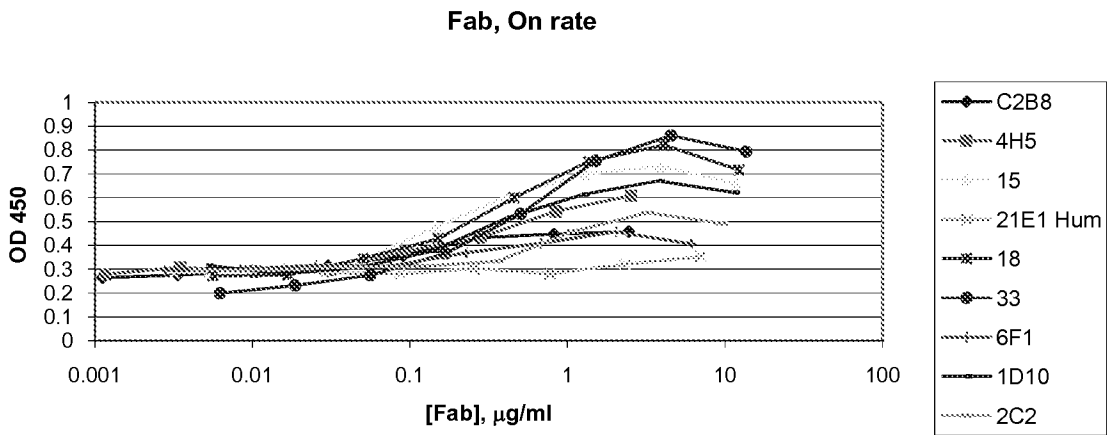
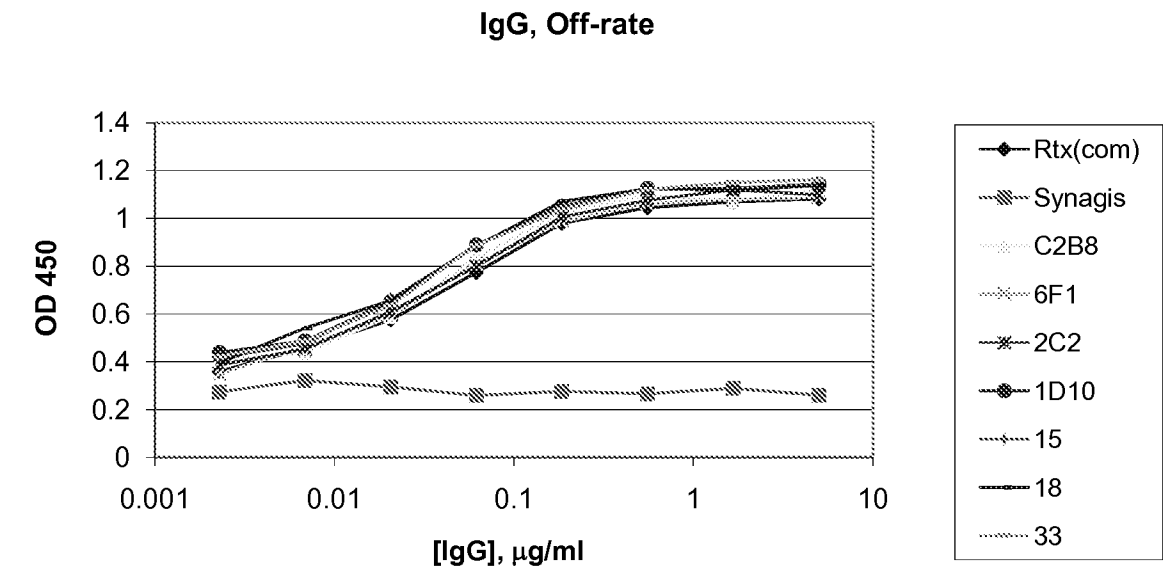
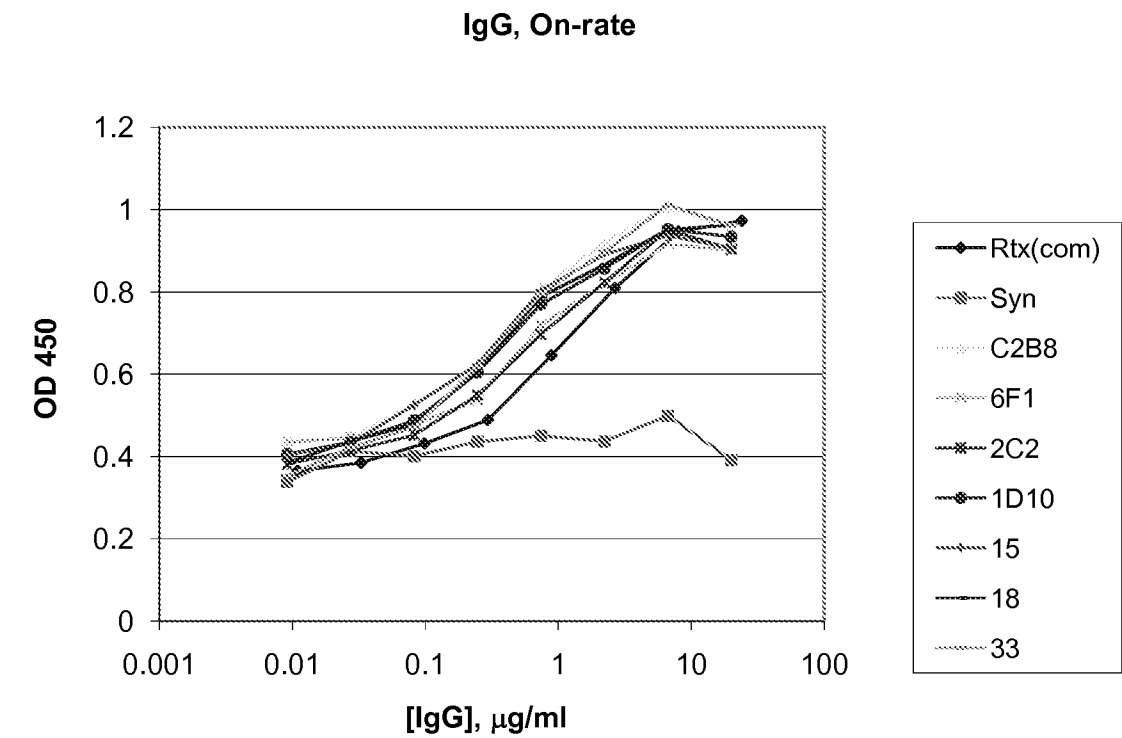


FIGURE 9

A.



B.

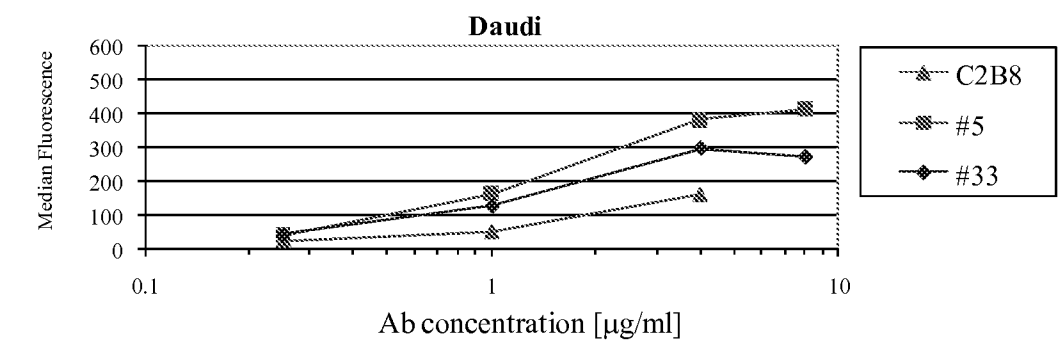




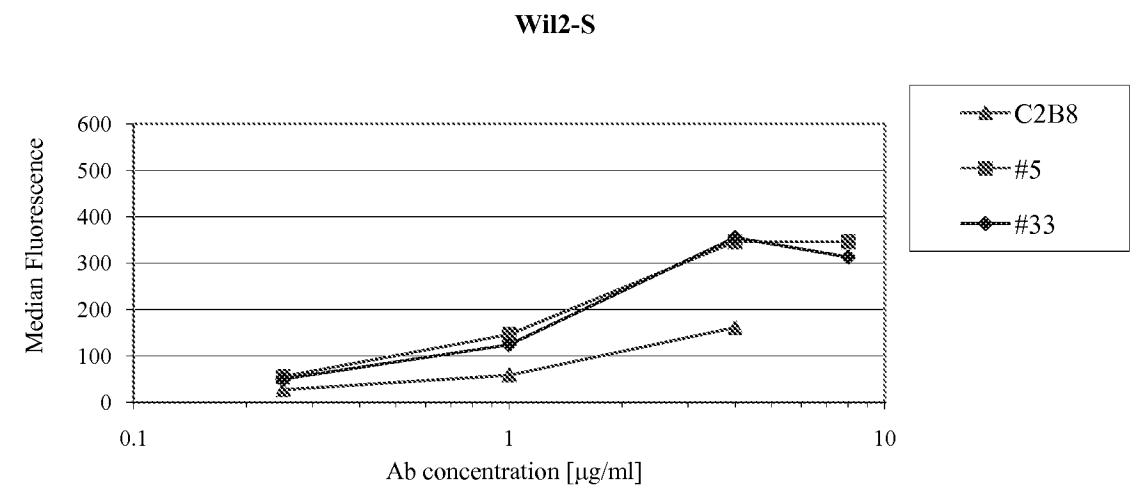
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FIGURE 10

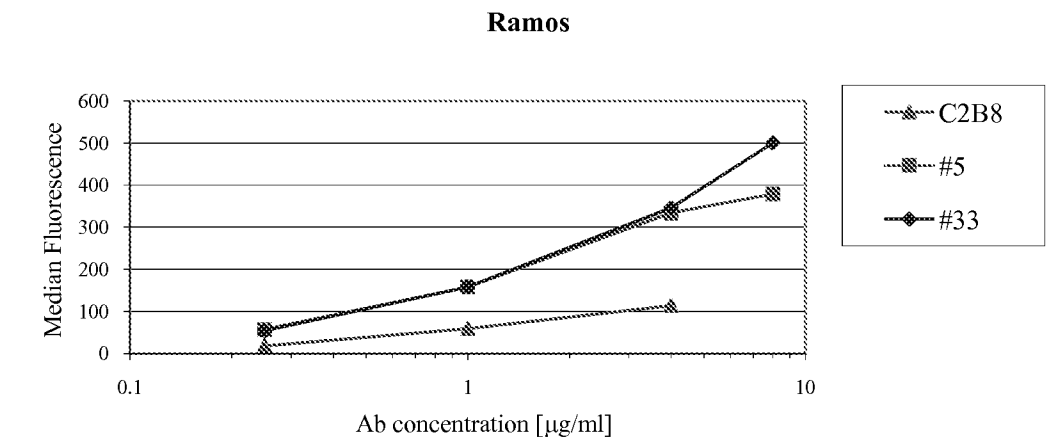
A.



B.



C.



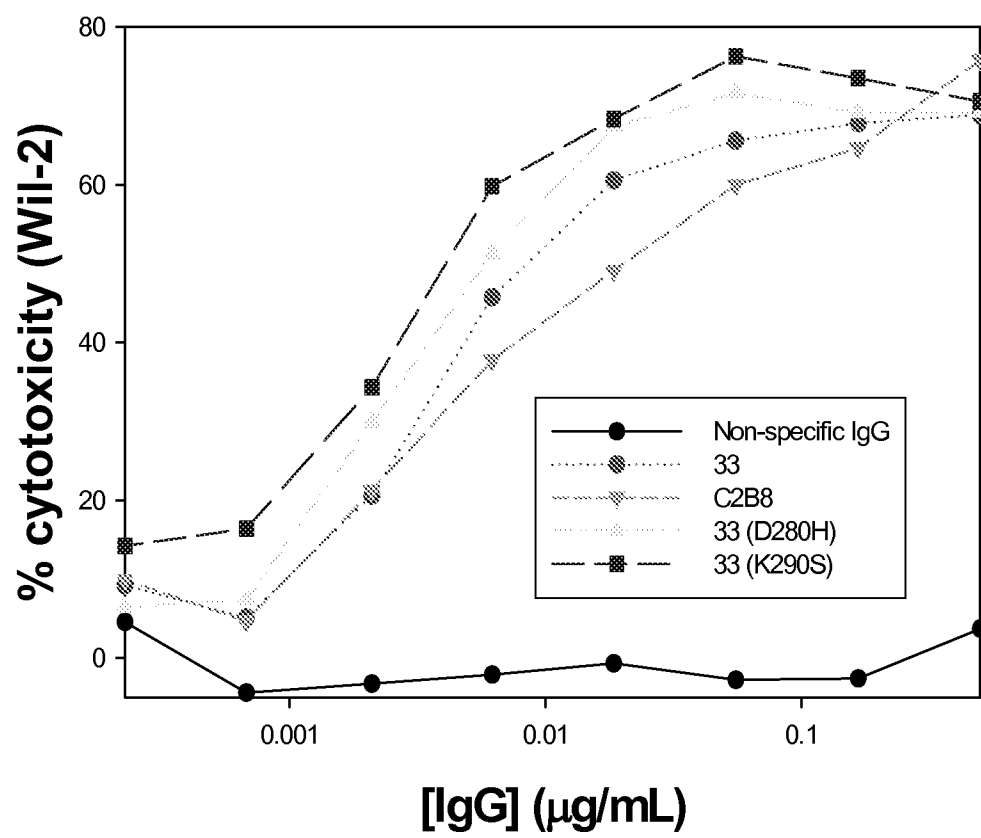
**FIGURE 11**

FIGURE 12

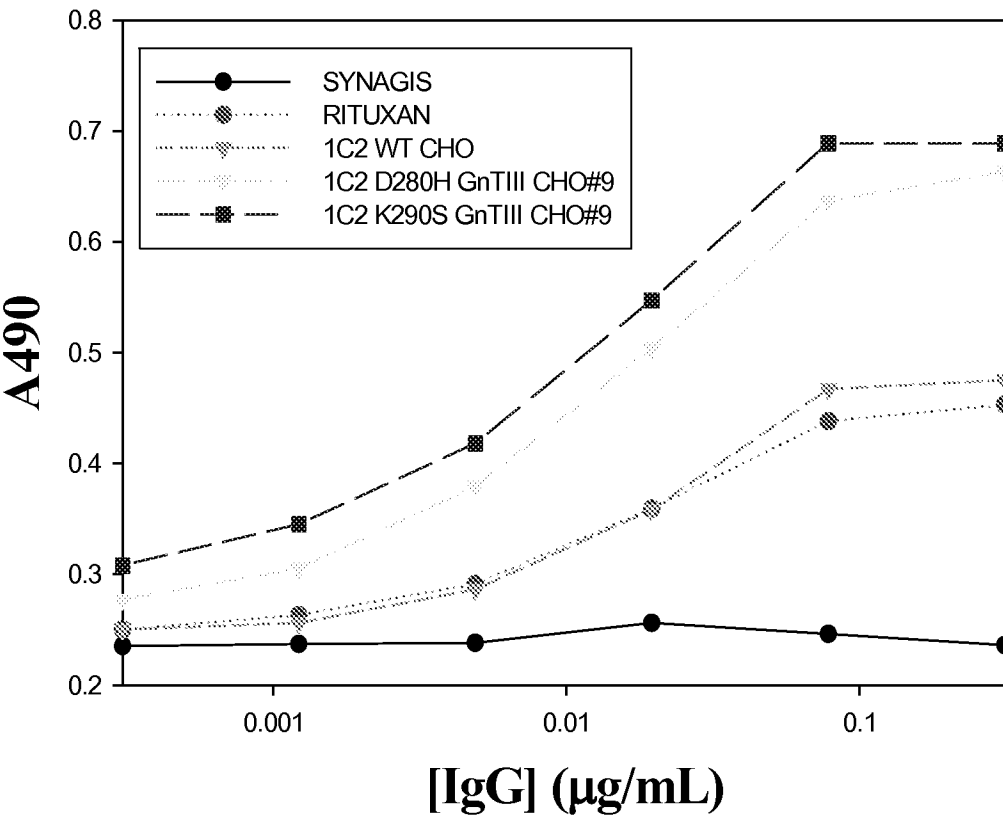


FIGURE 13

